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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=31; hr=16; min=58; sec=6; ms=464;]

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Reviewer Comments:

Sequence Listing

SEQUENCE LISTING

Please show "SEQUENCE LISTING" only once, at the top of the sequence listing.

<210> 8

<211> 85

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 8

ATGGCCAAGA CAATTGCTCG AGGGGATCCG GGCCCGAGCG AGGAGCCCGG TCCCTTTGTG 60

GGGCCGGGCT CCTCTGGTTG GTACC

85

Please convert the nucleotides above to lower-case letters. Since the submitted sequence listing is in ST.25 format, all nucleotides must be in lower-case letters. Same error in Sequences 9-12.

Application No: 10524586 Version No: 2.0

Input Set:

Output Set:

Started: 2008-07-25 22:57:51.202
Finished: 2008-07-25 22:57:53.346
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 144 ms
Total Warnings: 212
Total Errors: 0
No. of SeqIDs Defined: 13
Actual SeqID Count: 13

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 112	Upper case found in data; Found at position(0) SeqId(8)
W 112	Upper case found in data; Found at position(1) SeqId(8)
W 112	Upper case found in data; Found at position(2) SeqId(8)
W 112	Upper case found in data; Found at position(3) SeqId(8)
W 112	Upper case found in data; Found at position(4) SeqId(8)
W 112	Upper case found in data; Found at position(5) SeqId(8)
W 112	Upper case found in data; Found at position(6) SeqId(8)
W 112	Upper case found in data; Found at position(7) SeqId(8)
W 112	Upper case found in data; Found at position(8) SeqId(8)
W 112	Upper case found in data; Found at position(9) SeqId(8)
W 112	Upper case found in data; Found at position(10) SeqId(8)
W 112	Upper case found in data; Found at position(11) SeqId(8)

Input Set:

Output Set:

Started: 2008-07-25 22:57:51.202
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Total Warnings: 212
Total Errors: 0
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Actual SeqID Count: 13

Error code	Error Description
W 112	Upper case found in data; Found at position(12) SeqId(8)
W 112	Upper case found in data; Found at position(13) SeqId(8)
W 112	Upper case found in data; Found at position(14) SeqId(8)
W 112	Upper case found in data; Found at position(15) SeqId(8)
W 112	Upper case found in data; Found at position(16) SeqId(8)
W 112	Upper case found in data; Found at position(17) SeqId(8)
W 112	Upper case found in data; Found at position(18) SeqId(8)
W 112	Upper case found in data; Found at position(19) SeqId(8) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)

Sequence Listing

SEQUENCE LISTING

<110> HONDA, Mitsuo
MATSUO, Kazuhiro
KANEKIYO, Masaru

<120> A recombinant BCG vaccine

<130> 2005-0221A/JFW/00653

<140> 10524586

<141> 2005-03-31

<150> JP2002-237610

<151> 2002-08-16

<160> 13

<210> 1

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 1

aatggatcct atagtgcaga acctc 25

<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 2

aatgggccct tacaaaactc ttgctttatg g 31

<210> 3

<211> 706

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (5)..(700)

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 3

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  Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
    1             5             10             15

tcg ccg cgc acc ctg aac gcc tgg gtc aag gtc gtc gag gag aag gcc 97
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala
      20             25             30

ttc tcg ccg gag gtc atc ccg atg ttc tcg gcc ctg tcg gag ggc gcc 145
Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
      35             40             45

acc ccg cag gac ctg aac acc atg ctg aac acc gtc ggc ggc cac cag 193
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
      50             55             60

gcc gcc atg cag atg ctg aag gag acc atc aac gag gag gcc gcc gag 241
Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
      65             70             75

tgg gac cgc ctg cac ccg gtc cac gcc ggc ccc atc gca ccg ggc cag 289
Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
      80             85             90             95

atg cgc gag cct cgc ggc tcg gac atc gcc ggc acc acc tcg acc ctc 337
Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
      100            105            110

cag gag cag atc ggc tgg atg acc cac aac ccg ccg atc ccg gtc ggc 385
Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile Pro Val Gly
      115            120            125

gag atc tac aag cgc tgg atc atc ctg ggc ctg aac aag atc gtc cgc 433
Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
      130            135            140

atg tac tcg ccg acc tcg atc ctg gac atc cgc cag ggt ccg aag gag 481
Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
      145            150            155

ccg ttc cgc gac tac gtc gac cgc ttc tac aag acc ctc cgc gcc gag 529
Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
      160            165            170            175

cag gcg tcg cag gag gtc aag aac tgg atg acc gag acc ctg ctg gtc 577
Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
      180            185            190

cag aac gcc aac ccg gac tgc aag acc atc ctg aag gcc ctg ggt ccg 625
Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
      195            200            205

ggc gcc acc ctg gag gag atg atg acc gcc tgc cag ggc gtc ggc ggc 673
Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
      210            215            220
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ccg ggc cac aag gcg cgc gtc ctg taa gggccc

706

Pro Gly His Lys Ala Arg Val Leu

225

230

<210> 4

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligopeptide

<400> 4

Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu

1

5

10

15

<210> 5

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligopeptide

<400> 5

Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr

1

5

10

15

<210> 6

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligopeptide

<400> 6

Met Ala Lys Thr Ile

1

5

<210> 7

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligopeptide

<400> 7

Met Ala Lys Thr Ile Ala Arg Gly Asp Pro Ile Val Gln

1

5

10

<210> 8
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 8
ATGGCCAAGA CAATTGCTCG AGGGGATCCG GGCCCGAGCG AGGAGCCCGG TCCCTTTGTG 60

GGGCCGGGCT CCTCTGGTTG GTACC 85

<210> 9
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 9
ATGGCCAAGA CAATTGCTCG AGGGGATCCG ATCGTGCAG 39

<210> 10
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 10
ATGGCCAAGA CAATTGCTCG AGGGGATCCT ATAGTGCAG 39

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 11
CGCGTCCTGT AAGGGCCC 18

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 12

AGAGTTTTGT AAGGGCCC

18

<210> 13

<211> 706

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (5)..(700)

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 13

ggat cct ata gtg cag aac ctc cag ggg caa atg gta cat cag gcc ata 49

Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile

1

5

10

15

tca cct aga act tta aat gac tgg gta aaa gta gta gaa gag aag gtt 97

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala

20

25

30

ttc agc cca gaa gta ata ccc atg ttt tca gca tta tca gaa gga gcc 145

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala

35

40

45

acc cca caa gat tta aat acc atg cta aac aca gtg ggg gga cat caa 193

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln

50

55

60

gca gcc atg caa atg tta aaa gag acc atc aat gag gaa gct gca gaa 241

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu

65

70

75

tgg gat aga ttg cat cca gtg cat gca ggg cct att gca cca ggc cag 289

Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln

80

85

90

95

atg aga gaa cca agg gga agt gac ata gca gga act act agt acc ctt 337

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu

100

105

110

cag gaa caa ata gga tgg atg aca cat aat cca cct atc cca gta gga 385

Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile Pro Val Gly

115

120

125

gaa atc tat aaa aga tgg ata atc ctg gga tta aat aaa ata gta aga 433

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg

130

135

140

atg tat agc cct acc agc att ctg gac ata aga caa gga cca aag gaa 481

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu

145	150	155	
ccc ttt aga gac tat gta gac cga ttc tat aaa act cta aga gcc gag	529		
Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu			
160	165	170	175
caa gct tca caa gag gta aaa aat tgg atg aca gaa acc ttg ttg gtc	577		
Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val			
180	185	190	
caa aat gcg aac cca gat tgt aag act att tta aaa gca ttg gga cca	625		
Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro			
195	200	205	
gga gcg aca cta gaa gaa atg atg aca gca tgt cag gga gtg ggg gga	673		
Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly			
210	215	220	
ccc ggc cat aaa gca aga gtt ttg taa gggccc	706		
Pro Gly His Lys Ala Arg Val Leu			
225	230		